Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in this application:

Claims 1-45 (cancelled).

Claim 46 (currently amended). A method for ~~of~~ identifying an aptamer that binds to a target[[,]] wherein ~~the~~ binding of the aptamer to the target increases the binding affinity of the target for a target partner comprising the ~~following~~ steps:

a) contacting a candidate mixture of nucleic acids with the [[a]] target partner or target partner analog or both under conditions that favor specific binding between the nucleic acids and the target partner or target partner analog or both;

b) partitioning the bound nucleic acids from the unbound nucleic acids, and retaining the unbound nucleic acids;

c) contacting the unbound nucleic acids with the target and the target partner or target partner analog or both under conditions that disfavor efficient binding between the target and the target partner or target partner analog or both;

d) partitioning nucleic acids bound to a target-target partner complex or a target-target partner analog complex or both from unbound nucleic acids; and

e) retaining the nucleic acids bound to the target-target partner complex or the target-target partner analog complex or both,

thereby identifying an aptamer that binds to a target wherein ~~the~~ binding of the aptamer to the target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claim 47 (currently amended). A method for ~~of~~ identifying an aptamer that binds to a target[[~~,~~]] wherein ~~the~~ binding of the aptamer to the target increases the binding affinity of the target for a target partner comprising the ~~following~~ steps:

a) contacting a target-specific ~~target-based~~ pool of nucleic acid molecules having high affinity and specificity for the target with the target and the [[a]] target partner or target partner analog or both under conditions that disfavor efficient binding between the target and the [[a]] target partner or target partner analog or both, wherein the target partner or target partner analog or both is attached to a support;

b) partitioning nucleic acids bound to the support bound target-target partner complex or target-target partner analog complex or both from unbound nucleic acids; and

c) retaining the nucleic acids associated with the support bound target-target partner complex or target-target partner analog complex or both,

thereby identifying an aptamer that binds to a target wherein ~~the~~ binding of the aptamer to the target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claim 48 (currently amended). The method of claim 46, wherein the candidate mixture of nucleic acids ~~in step a)~~ is a target-specific ~~target-based~~ pool of nucleic acid molecules having high affinity and specificity for the target.

Claim 49 (currently amended). The method of claim 46 or 48, wherein step e) further comprises removing the retained nucleic acids from the target-target partner complex or target-target partner analog complex or both.

Claim 50 (currently amended). The method of claim 47, wherein step c) further comprises removing the retained nucleic acids from the target-target partner complex or target-target partner analog complex or both.

Claim 51 (currently amended). The method of claim 49, further comprising ~~in step e)~~ amplifying the removed nucleic acid molecules and repeating steps a) to e).

Claim 52 (currently amended). The method of claim 50, further comprising ~~repeating in step c)~~ amplifying the removed nucleic acid molecules and repeating steps a) to c).

Claim 53 (currently amended). The method of claim 51, wherein the target partner or target partner analog or both is ~~are~~ immobilized.

Claim 54 (currently amended). The method of claim 48 ~~51~~, wherein the target-specific ~~target-based~~ pool of nucleic acid molecules is diversified.

Claim 55 (currently amended). The method of claim 47, wherein step [[(]]c) further comprises removing the nucleic acids ~~molecules~~ from the target-target partner complex or target-target partner analog complex or both by eluting the nucleic acids ~~aptamer~~ with an agonist competitor to the target ~~aptamer~~.

Claim 56 (currently amended). The method of claim 46 ~~49~~, wherein step [[(]]e) further comprises removing the nucleic acids ~~molecules~~ from the target-target partner complex or target-target partner analog complex or both by eluting the nucleic acids ~~aptamer~~ with an agonist competitor to the target ~~aptamer~~.

Claim 57 (currently amended). The method of claim 49, wherein step [[(]]e) further comprises contacting the bound nucleic acids with excess free target.

Claims 58-59 (cancelled).

Claim 60 (currently amended). A method for ~~of~~ identifying an aptamer that binds to a target[[,]] wherein ~~the~~ binding of the aptamer to the target increases the binding affinity of the target for a target partner[[,]] comprising the ~~following~~ steps:

a) contacting a candidate mixture of nucleic acids with a target partner or target partner analog or both under conditions that favor specific binding between the nucleic acids and the target partner or target partner analog or both;

b) partitioning the bound nucleic acids from the unbound nucleic acids, and retaining the unbound nucleic acids;

c) binding the target to the ~~a~~ target partner or target partner analog or both to form a target-target partner complex or target-target partner analog complex or both, and contacting the target-target partner complex or target-target partner analog complex or both with the unbound nucleic acids under conditions that favor specific binding between the nucleic acids and the target-target partner complex or target-target partner analog complex or both; and

d) removing nucleic acids with low binding affinity for the target-target partner complex or target-target partner analog complex or both; and

e) combining an agonist competitor with the nucleic acids bound to the target-target partner complex or target-target partner analog complex or both, and eluting the bound nucleic acids,

thereby identifying an aptamer that binds to a target wherein ~~the~~ binding of the aptamer to the target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claim 61 (currently amended). The method of claim 60, further comprising ~~in step e)~~ amplifying the eluted nucleic acids and repeating steps a) to e).

Claim 62 (currently amended). The method of claim 60 ~~61~~, wherein the candidate mixture of nucleic acids ~~in step a)~~ is a target-specific ~~target-based~~ pool of nucleic acid molecules having high affinity and specificity for the target.

Claim 63 (currently amended). The method of claim 62, wherein the target-specific ~~target-based~~ pool of nucleic acid molecules is diversified.

Claim 64 (currently amended). The method of claim 60, wherein the target-target partner complex or target-target partner analog complex or both is immobilized.

Claim 65 (cancelled).

Claim 66 (currently amended). A method for ~~of~~ identifying an aptamer that binds to a target[[~~,~~]] wherein ~~the~~ binding of the aptamer to the target increases the binding affinity of the target for a target partner comprising the ~~following~~ steps:

a) contacting a candidate mixture of nucleic acids with the [[a]] target partner or target partner analog or both;

b) partitioning the bound nucleic acids from the unbound nucleic acids, and retaining the unbound nucleic acids;

c) contacting the unbound nucleic acids with the target and the target partner or target partner analog or both under conditions that disfavor efficient ~~specific~~ binding of the target to the target partner or target partner analog or both;

d) partitioning the unbound nucleic acids and the nucleic acids bound to ~~either~~ the target ~~partner or target partner analog~~ from the nucleic acids bound to a ~~the~~ target-target partner complex or target-target partner analog complex or both; and

e) ~~removing and~~ retaining the nucleic acids bound to the target-target partner complex or target-target partner analog complex or both,

thereby identifying an aptamer that binds a target wherein ~~the~~ binding of the aptamer to the target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claims 67-68 (cancelled).

Claim 69 (currently amended). A method for ~~of~~ identifying an aptamer that binds to a target[~~,~~] wherein ~~the~~ binding of the aptamer to the target increases the binding affinity of the target for a target partner[[,]] comprising the ~~following~~ steps:

a) binding the target to the target partner or target partner analog or both to form a target-target partner complex or target-target partner analog complex or both, and contacting the target-target partner complex or target-target partner analog complex or both with a target-specific ~~target-based~~ pool of nucleic acid molecules having high affinity and specificity for the target under conditions that favor specific binding between the nucleic acids and the target-target partner complex or target-target partner analog complex or both; and

b) removing nucleic acids with low binding affinity for the target-target partner complex or target-target partner analog complex or both; and

c) retaining the target-target partner complex or target-target partner analog complex or both with bound nucleic acids; and

d) combining an agonist competitor with the nucleic acids bound to the target-target partner complex or target-target partner analog complex or both, eluting the bound nucleic acids[[,]] and amplifying the eluted nucleic acids,

thereby identifying an aptamer that binds to a target[[,]] wherein ~~the~~ binding of the aptamer to the target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claim 70 (currently amended). The method of claim 69, further comprising the steps of: contacting a modified target, wherein the modified target is lacking a region or regions required for ~~the~~ binding of the target to the target partner or target partner analog or both, with a pool of nucleic acid molecules; partitioning the bound nucleic acids from the unbound nucleic acids; and contacting the unbound nucleic acids with the complex in step a).

Claim 71 (currently amended). The method of claim 70, wherein the pool of nucleic acid molecules comprises a target-specific ~~target-based~~ pool of nucleic acid molecules having high affinity and specificity for the target.

Claim 72 (previously presented). The method of claim 46, further comprising step f) screening the nucleic acids retained in step e) for a desired functional activity.

Claim 73 (currently amended). The method of claim 46, further comprising the steps of: contacting a modified target, wherein the modified target is lacking a region or regions required for ~~the~~ binding of the target to the target partner or target partner analog or both, with a pool of nucleic acid molecules; partitioning the bound nucleic acids from the unbound nucleic acids; and contacting the unbound nucleic acids with the target and target partner or target partner analog or both ~~complex~~ in step c) ~~a)~~.

Claim 74 (currently amended). The method of claim 73, wherein the candidate mixture ~~pool~~ of nucleic acids ~~molecules~~ comprises a target-specific ~~target-based~~ pool of nucleic acid molecules having high affinity and specificity for the target.

Claim 75 (currently amended). The method of claim 46, wherein ~~the~~ binding of the aptamer to the target exposes a portion of the target, wherein the ~~said~~ exposed portion of the target has an increased binding affinity for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claim 76 (currently amended). The method of claim 46, wherein ~~the~~ binding of the aptamer to the target induces a conformational change in the target that ~~which~~ increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claim 77 (currently amended). The method of claim 47, wherein the support is ~~target partner or target partner analog or both are~~ immobilized.

Claim 78 (currently amended). The method of claim 47, wherein the target-specific ~~target-based~~ pool of nucleic acid molecules is diversified.

Claim 79 (currently amended). The method of claim 47, wherein step [[(]]c) further comprises contacting the bound nucleic acids with excess free target.

Claim 80 (previously presented). The method of claim 47, further comprising step d) screening the nucleic acids retained in step c) for a desired functional activity.

Claim 81 (currently amended). The method of claim 47, further comprising the steps of: contacting a modified target, wherein the modified target is lacking a region or regions required for ~~the~~ binding of the target to the target partner or target partner analog or both, with a pool of nucleic acid molecules; partitioning the bound nucleic acids from the unbound nucleic acids; and contacting the unbound nucleic acids with the target and the target partner or target partner analog or both ~~complex~~ in step a).

Claim 82 (currently amended). The method of claim 81, wherein the pool of nucleic acid molecules comprises a target-specific ~~target-based~~ pool of nucleic acid molecules having high affinity and specificity for the target.

Claim 83 (currently amended). The method of claim 47, wherein ~~the~~ binding of the aptamer to the target exposes a portion of the target, wherein the ~~said~~ exposed portion of the

target has an increased binding affinity for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claim 84 (currently amended). The method of claim 47, wherein ~~the~~ binding of the aptamer to the target induces a conformational change in the target that ~~which~~ increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

Claim 85 (currently amended). The method of claim 60, wherein step e) further comprises removing the retained nucleic acids from the target-target partner complex or target-target partner analog complex or both.

Claim 86 (currently amended). The method of claim 60, wherein step [[(]]e) further comprises contacting the bound nucleic acids with excess free target.

Claim 87 (currently amended). The method of claim 60, further comprising step f) screening the nucleic acids eluted ~~amplified~~ in step e) for a desired functional activity.

Claim 88 (currently amended). The method of claim 60, further comprising the steps of: contacting a modified target, wherein the modified target is lacking a region or regions required for ~~the~~ binding of the target to the target partner or target partner analog or both, with a pool of nucleic acid molecules; partitioning the bound nucleic acids from the unbound nucleic acids; and contacting the unbound nucleic acids with the complex in step a).

Claim 89 (currently amended). The method of claim 88, wherein the pool of nucleic acid molecules comprises a target-specific ~~target-based~~ pool of nucleic acid molecules having high affinity and specificity for the target.

Claim 90 (currently amended). The method of claim 60, wherein ~~the~~ binding of the aptamer to the target exposes a portion of the target, wherein the ~~said~~ exposed portion of the

target has an increased binding affinity for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claim 91 (currently amended). The method of claim 60, wherein ~~the~~ binding of the aptamer to the target induces a conformational change in the target that ~~which~~ increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claim 92 (currently amended). The method of claim 66, wherein step e) further comprises removing the retained nucleic acids from the target-target partner complex or target-target partner analog complex or both.

Claim 93 (currently amended). The method of claim 66, wherein step [[(]]e) further comprises contacting the bound nucleic acids with excess free target.

Claim 94 (previously presented). The method of claim 66, further comprising step f) screening the nucleic acids retained in step e) for a desired functional activity.

Claim 95 (currently amended). The method of claim 66, further comprising the steps of: contacting a modified target, wherein the modified target is lacking a region or regions required for ~~the~~ binding of the target to the target partner or target partner analog or both, with a pool of nucleic acid molecules; partitioning the bound nucleic acids from the unbound nucleic acids; and contacting the unbound nucleic acids with the complex in step a).

Claim 96 (currently amended). The method of claim 95, wherein the pool of nucleic acid molecules comprises a target-specific ~~target-based~~ pool of nucleic acid molecules having high affinity and specificity for the target.

Claim 97 (currently amended). The method of claim 66, wherein ~~the~~ binding of the aptamer to the target exposes a portion of the target, wherein the ~~said~~ exposed portion of the

target has an increased binding affinity for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claim 98 (currently amended). The method of claim 66, wherein ~~the~~ binding of the aptamer to the target induces a conformational change in the target that ~~which~~ increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claim 99 (currently amended). The method of claim 66, wherein the target partner or target partner analog or both is ~~are~~ immobilized.

Claim 100 (currently amended). The method of claim 66, further comprising ~~in step e)~~ amplifying the eluted nucleic acids and repeating steps a) to e).

Claim 101 (currently amended). The method of claim 66, where step e) further comprises removing the nucleic acid molecules from the target-target partner complex or target-target partner analog complex or both by eluting the molecules ~~aptamer~~ with an agonist competitor to the target ~~aptamer~~.

Claim 102 (currently amended). The method of claim 66, wherein the candidate mixture of nucleic acids ~~in step a)~~ is a target-specific ~~target-based~~ pool of nucleic acid molecules having high affinity and specificity for the target.

Claim 103 (currently amended). The method of claim 102, wherein the target-specific ~~target-based~~ pool of nucleic acid molecules is diversified.

Claim 104 (currently amended). The method of claim 69, wherein step d) further comprises removing the retained nucleic acids from the target-target partner complex or target-target partner analog complex or both.

Claim 105 (currently amended). The method of claim 69, wherein step [[(]]d) further comprises contacting the bound nucleic acids with excess free target.

Claim 106 (previously presented). The method of claim 69, further comprising step e) screening the nucleic acids amplified in step d) for a desired functional activity.

Claim 107 (currently amended). The method of claim 69, wherein ~~the~~ binding of the aptamer to the target exposes a portion of the target, wherein the ~~said~~ exposed portion of the target has an increased binding affinity for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claim 108 (currently amended). The method of claim 69, wherein ~~the~~ binding of the aptamer to the target induces a conformational change in the target that ~~which~~ increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claim 109 (currently amended). The method of claim 69, wherein the target partner or target partner analog or both is ~~are~~ immobilized.

Claim 110 (currently amended). The method of claim 69, further comprising ~~in step e) amplifying the eluted nucleic acids and~~ repeating steps a) to d)~~e)~~.

Claim 111 (currently amended). The method of claim 69, where step d) ~~e)~~ further comprises removing the nucleic acid molecules from the target-target partner complex or target-target partner analog complex or both by eluting the molecules ~~aptamer~~ with an agonist competitor to the target ~~aptamer~~.

Claim 112 (cancelled).

Claim 113 (currently amended). The method of claim 112, wherein the target-specific ~~target-based~~ pool of nucleic acid molecules is diversified.

Claim 114 (currently amended). A method for ~~of~~ identifying an aptamer that binds to a target[~~,~~] wherein ~~the~~ binding of the aptamer to the target increases the binding affinity of the target for a target partner comprising the ~~following~~ steps:

a) contacting a candidate mixture of nucleic acids with a complex of the target and an agonist competitor under conditions that favor specific binding between the nucleic acid and the target-agonist competitor complex;

b) partitioning the bound nucleic acids from the unbound nucleic acids, and retaining the unbound nucleic acids;

c) contacting the unbound nucleic acids with the target and the target partner or target partner analog or both under conditions that disfavor efficient ~~specific~~ binding of the target and the target partner or target partner analog or both;

d) partitioning the unbound nucleic acids from the bound nucleic acids; and

e) ~~removing and~~ retaining the bound nucleic acids from the target-target partner complex or target-target partner analog complex or both,

thereby identifying an aptamer that binds to a target wherein ~~the~~ binding of the aptamer to the target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claim 115 (currently amended). The method of claim 114, wherein the candidate mixture of nucleic acids ~~in step a)~~ is a target-specific ~~target-based~~ pool of nucleic acid molecules having high affinity and specificity for the target.

Claim 116 (currently amended). The method of claim 114, wherein step e) further comprises removing the retained nucleic acids from the target-target partner complex or target-target partner analog complex or both.

Claim 117 (currently amended). The method of claim 114, wherein step [[(]]e) further comprises removing the nucleic acid molecules from the target-target partner complex or target-target partner analog complex or both by eluting the molecules ~~aptamer~~ with an agonist competitor to the target ~~aptamer~~.

Claim 118 (currently amended). The method of claim 115, wherein the target-specific ~~target-based~~ pool of nucleic acid molecules is diversified.

Claim 119 (currently amended). The method of claim 114, wherein step [[(]]e) further comprises contacting the bound nucleic acids with excess free target.

Claim 120 (currently amended). The method of claim 114, wherein the target and [[,]] the target partner or target partner analog or both are ~~in step c) is~~ immobilized.

Claim 121 (previously presented). The method of claim 114, further comprising step f) screening the nucleic acids retained in step e) for a desired functional activity.

Claim 122 (currently amended). The method of claim 114, further comprising the steps of: contacting a modified target, wherein the modified target is lacking a region or regions required for ~~the~~ binding of the target to the target partner or target partner analog or both, with a pool of nucleic acid molecules; partitioning the bound nucleic acids from the unbound nucleic acids; and contacting the unbound nucleic acids with the complex in step a).

Claim 123 (currently amended). The method of claim 122, wherein the pool of nucleic acid molecules comprises a target-specific ~~target-based~~ pool of nucleic acid molecules having high affinity and specificity for the target.

Claim 124 (currently amended). The method of claim 114, wherein ~~the~~ binding of the aptamer to the target exposes a portion of the target, wherein the ~~said~~ exposed portion of the

target has an increased binding affinity for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claim 125 (currently amended). The method of claim 114, wherein ~~the~~ binding of the aptamer to the target induces a conformational change in the target that ~~which~~ increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner when ~~where~~ the target is not bound by the aptamer.

Claim 126 (currently amended). The method of claim 114, further comprising ~~in step e)~~ amplifying the eluted nucleic acids and repeating steps a) to e).